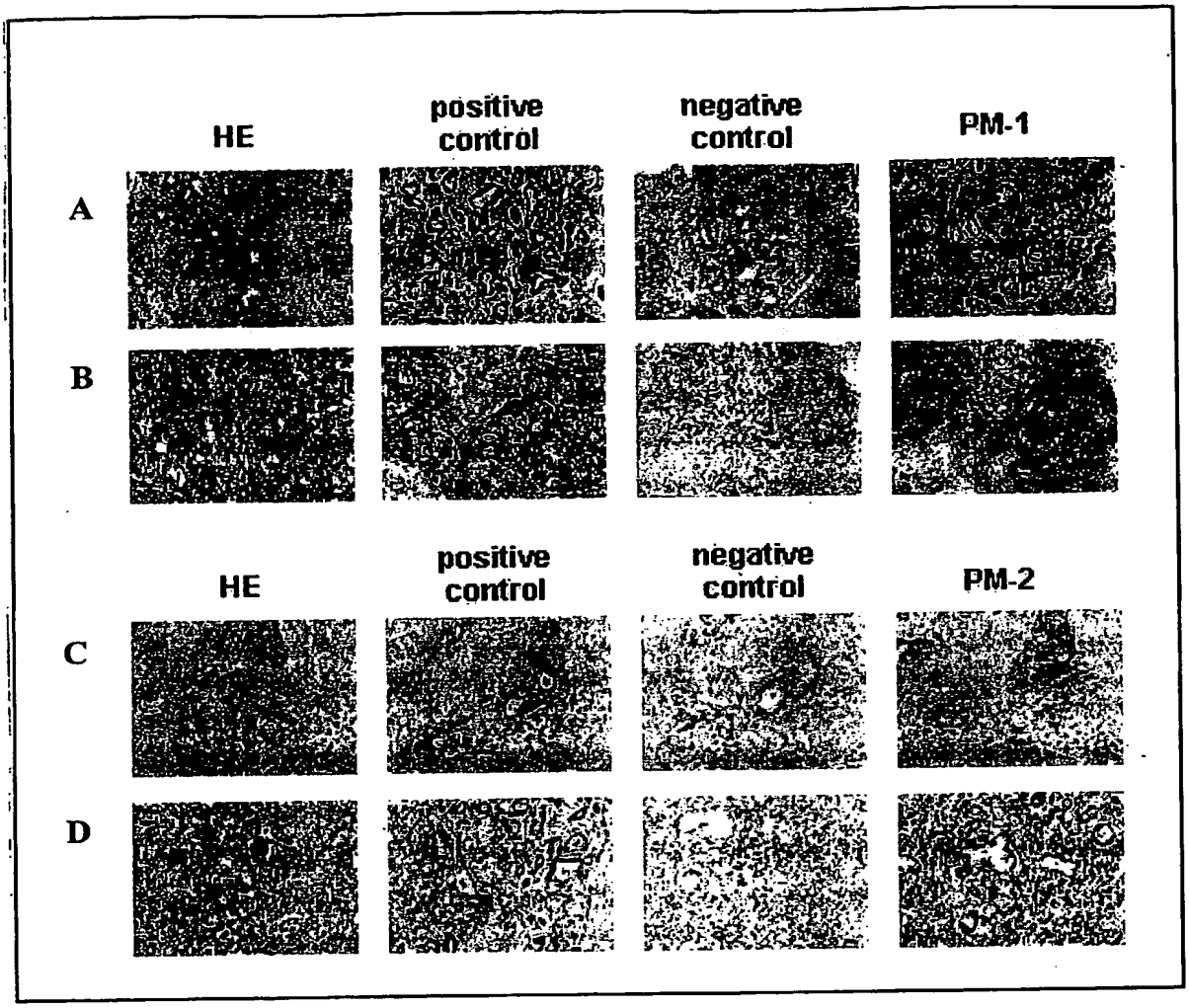


FIG. 1

BEST AVAILABLE COPY

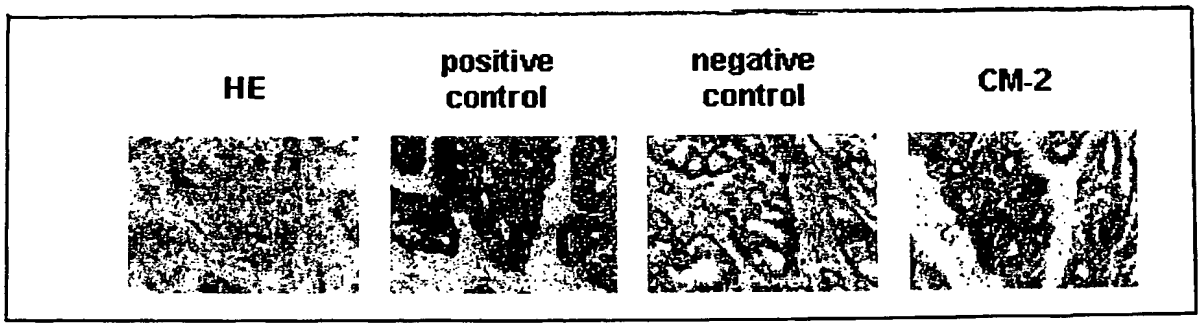
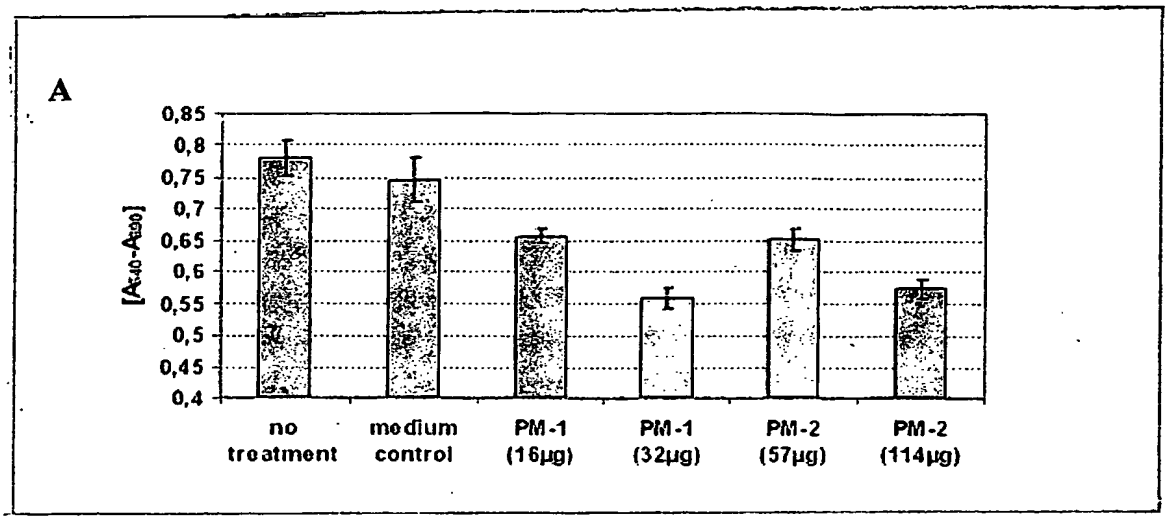


FIG. 2

BEST AVAILABLE COPY



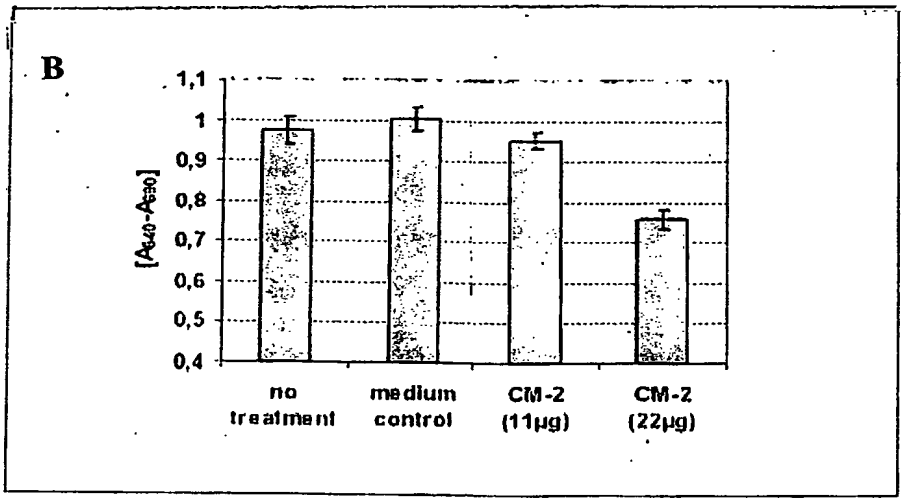
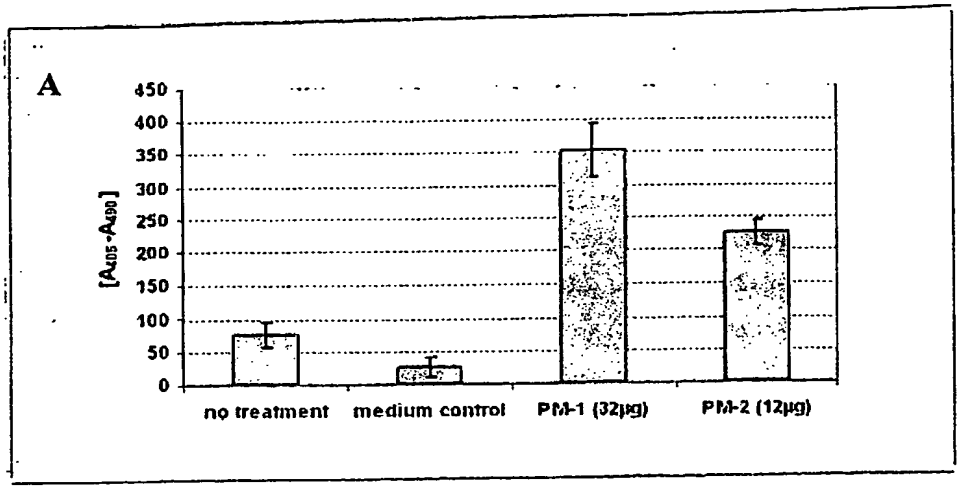


FIG. 3

BEST AVAILABLE COPY



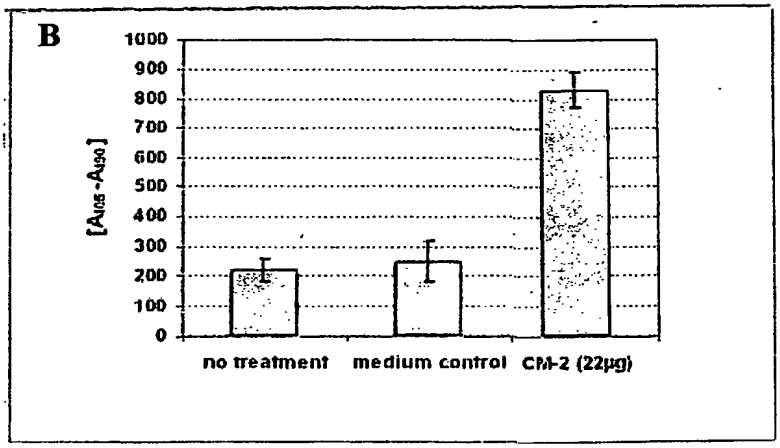


FIG. 4

BEST AVAILABLE COPY

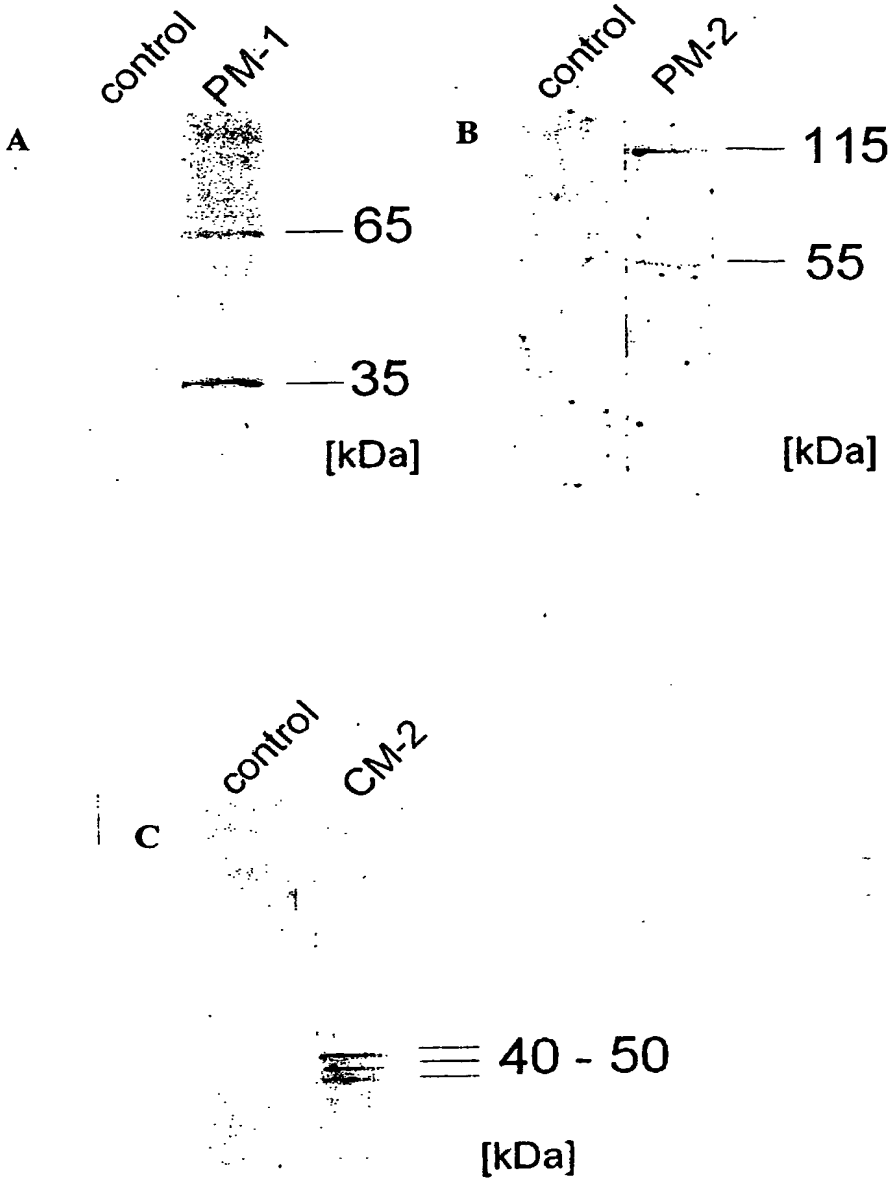


FIG. 5

BEST AVAILABLE COPY

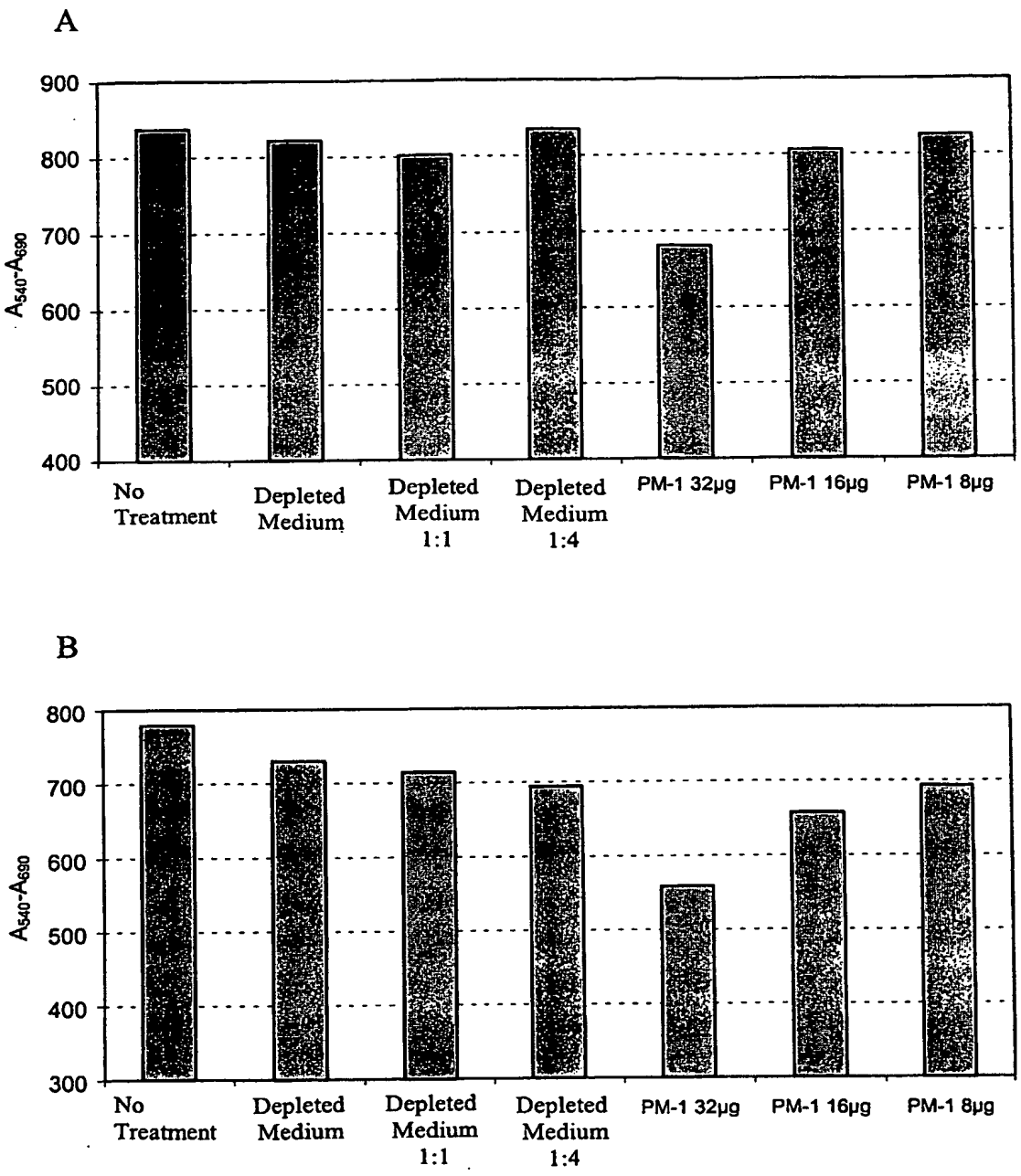


FIG. 6

BEST AVAILABLE COPY

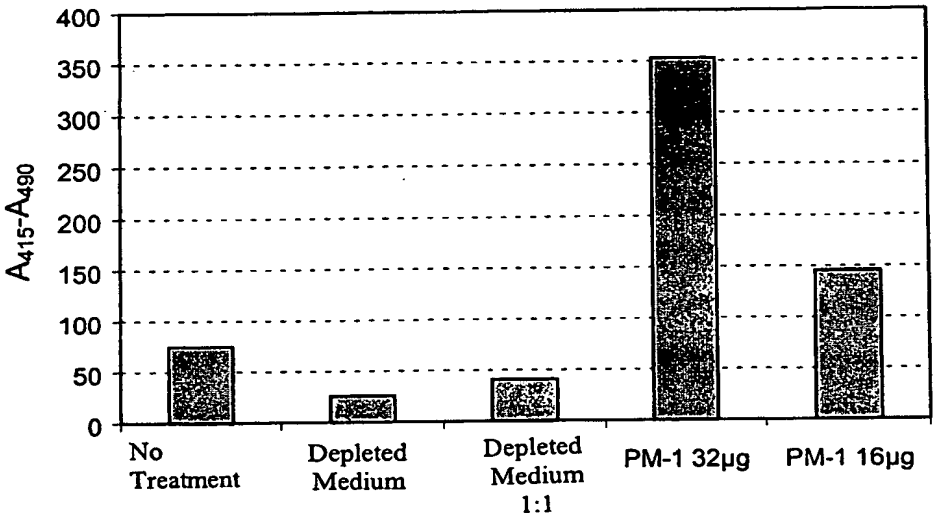
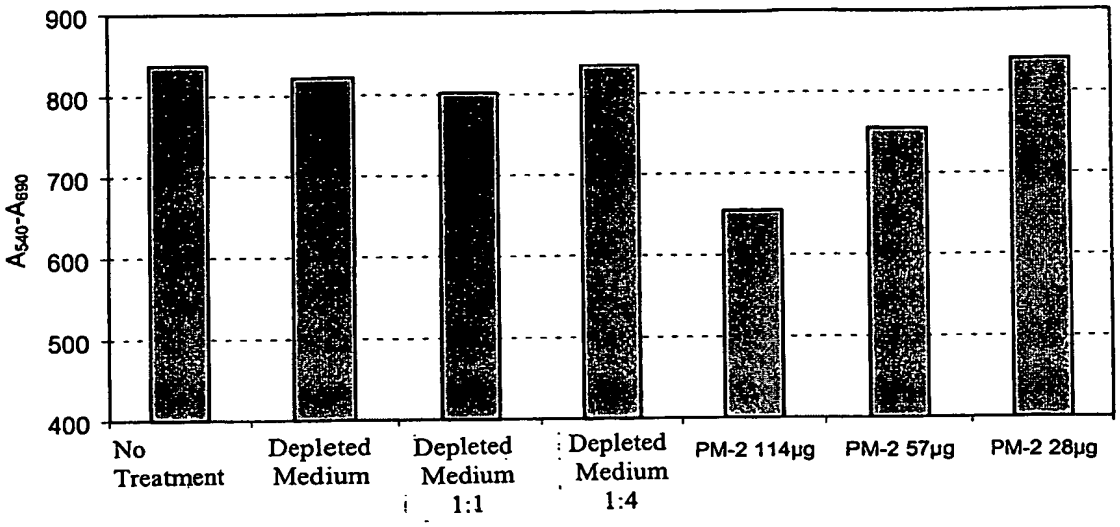

400
350
300
250
200
150
100
50
0
A_{415}-A_{490}
No Treatment
Depleted Medium
Depleted Medium 1:1
PM-1 32µg
PM-1 16µg

FIG. 7

A


900
800
700
600
500
400
A_{540}-A_{690}
No Treatment
Depleted Medium
Depleted Medium 1:1
Depleted Medium 1:4
PM-2 114µg
PM-2 57µg
PM-2 28µg

B

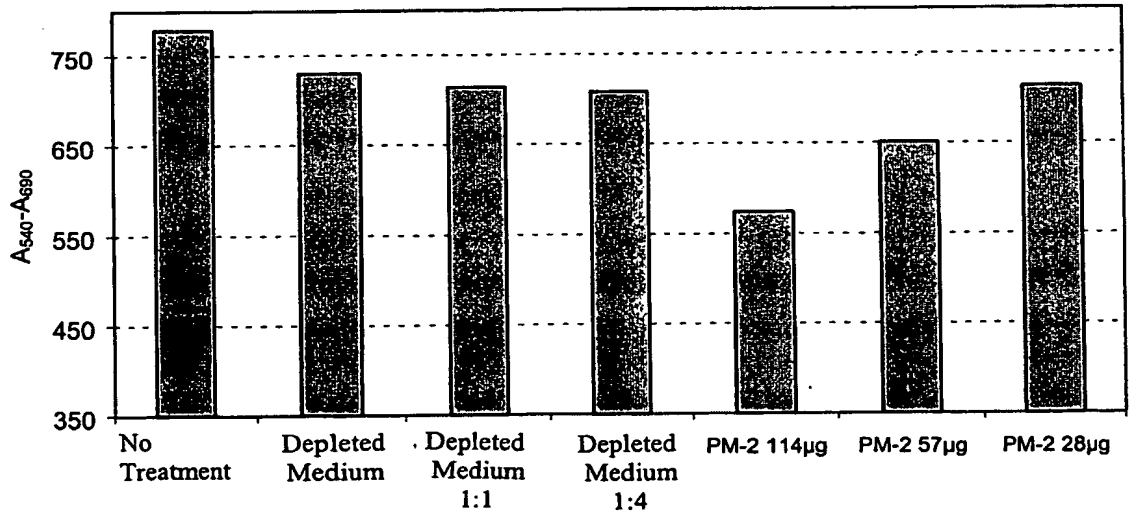

750
650
550
450
350
A_{540}-A_{690}
No Treatment
Depleted Medium
Depleted Medium 1:1
Depleted Medium 1:4
PM-2 114µg
PM-2 57µg
PM-2 28µg

FIG. 8

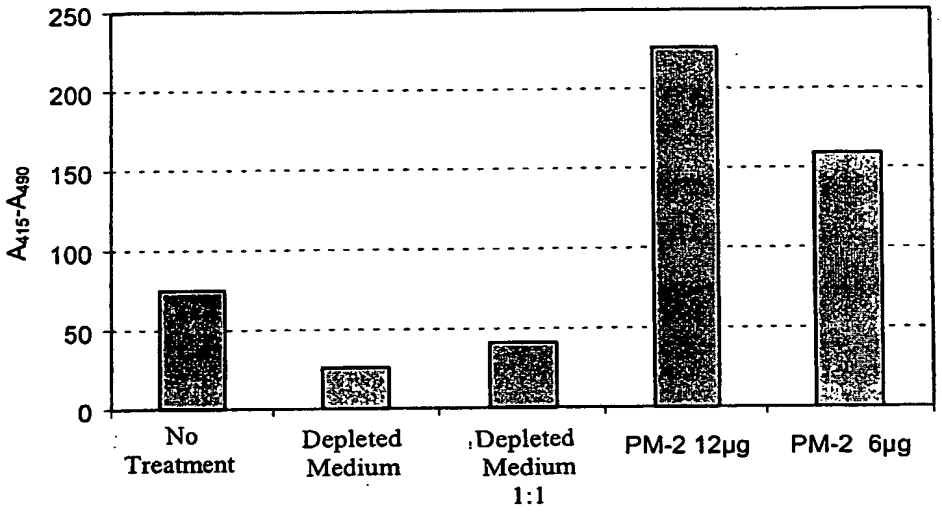

250
200
150
100
50
0
A415-A490
No Treatment
Depleted Medium
Depleted Medium 1:1
PM-2 12µg
PM-2 6µg

FIG. 9

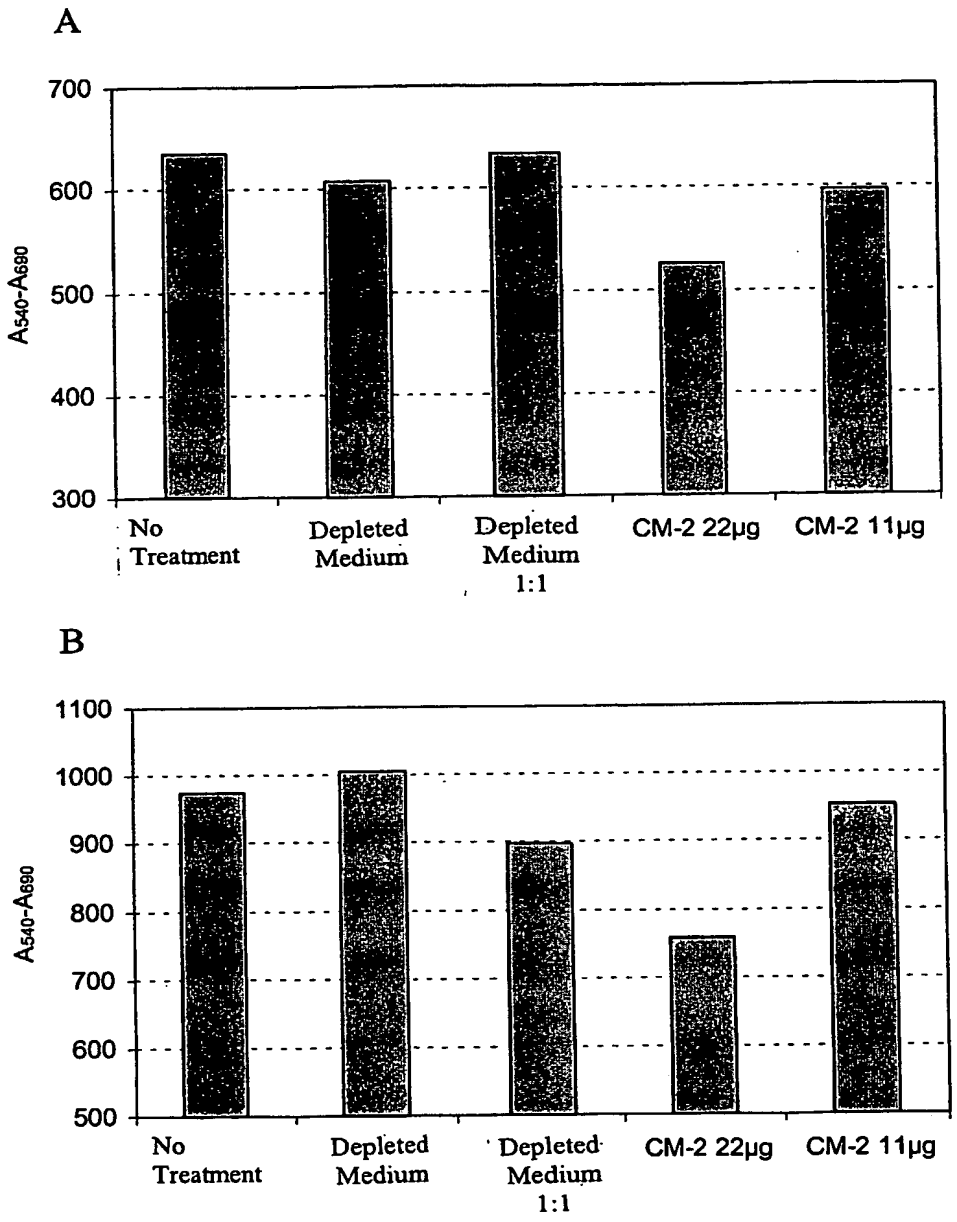

A
700
600
500
400
300
A540-A690
No Treatment
Depleted Medium
Depleted Medium 1:1
CM-2 22µg
CM-2 11µg
B
1100
1000
900
800
700
600
500
A540-A690
No Treatment
Depleted Medium
Depleted Medium 1:1
CM-2 22µg
CM-2 11µg

FIG. 10

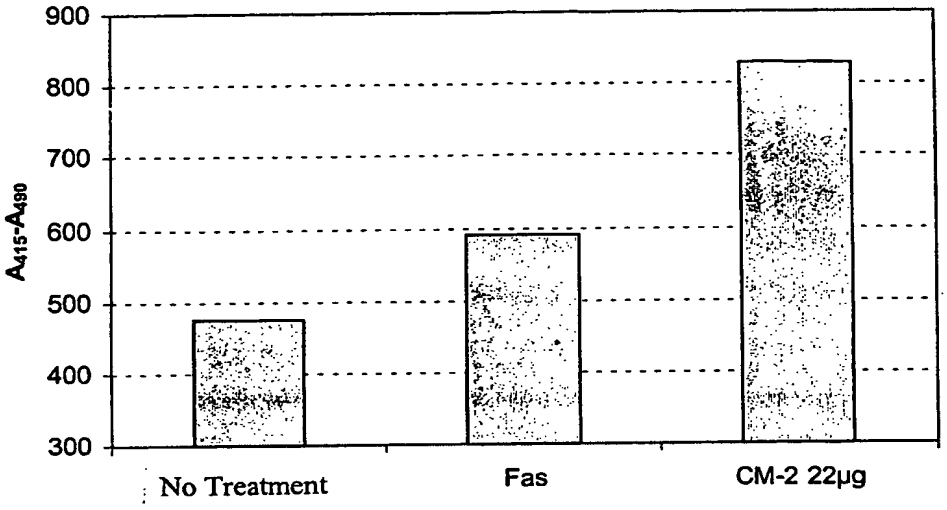

900
800
700
600
500
400
300
A_{415}-A_{490}
No Treatment
Fas
CM-2 22µg

FIG. 11

PM-1 Light chain variable region sequence

```
tcc tat gtg ctg act cag cca ccc tcg gtg tca gtg tcc cca gga caa acg gcc agg atc      60
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile
 1               5                  10                  15                  20

                          CDR1
acc tgc tct gga gat gca ttg cca aaa aaa tat cct tat tgg tac cag cag aag tca ggc     120
Thr Cys Ser Gly Asp Ala Leu Pro Lys Lys Tyr Pro Tyr Trp Tyr Gln Gln Lys Ser Gly
                25                  30                  35                  40

                                CDR2
cag gcc cct gtg ctg gtc atc tat gag gac agc aaa cga ccc tcc ggg atc cct gag aga     180
Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
                45                  50                  55                  60

ttc tct ggc tcc agc tca ggg aca atg gcc acc ttg act atc agt ggg gcc cag gtg gag     240
Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu
                65                  70                  75                  80

                                CDR3
gat gaa gct gac tac tac tgt tac tca aca gac agc agt ggt aat atg tct tcg gaa ctg     300
Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Thr Asp Ser Ser Gly Asn Met Ser Ser Glu Leu
                85                  90                  95                  100

gga cca agc tca ccg tcc                                                           318
Gly Pro Ser Ser Pro Ser
                105
```

FIG. 12

PM-1 Heavy chain variable region sequence

CDR1

```
ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agc tat gcc atg agc      60
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
 1               5                  10                  15                  20

                                                                  CDR2
tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca gct att agt ggt agt ggt     120
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly
                25                  30                  35                  40

ggt agc aca tac tac gca gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc     180
Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                45                  50                  55                  60

aag aac acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac     240
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                65                  70                  75                  80

        CDR3
tgt gcg aaa gat tca ttt cgt gaa gga ccc tgg ggc cag gga acc ctg gtc acc           294
Cys Ala Lys Asp Ser Phe Arg Glu Gly Pro Trp Gly Gln Gly Thr Leu Val Thr
                85                  90                  95
```

FIG. 13

PM-2 Light chain variable region sequence

```
cag tct gcc ctg act cag cct gct tcc ctc tct gca tct cct gga gca tca gcc agt ctc      60
Gln Ser Ala Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu
 1               5                  10                  15                  20

                                CDR1
                  ---------------------------------
acc tgc acc ttg cgc agt ggc atc aat gtt ggt acc tac agg ata tac tgg tac cag cag      120
Thr Cys Thr Leu Arg Ser Gly Ile Asn Val Gly Thr Tyr Arg Ile Tyr Trp Tyr Gln Gln
                25                  30                  35                  40

                                                CDR2
                                    ---------------------------------
aag cca ggg agt cct ccc cag tat ctc ctg agg tac aaa tca gac tca gat aag cag aag      180
Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Lys
                45                  50                  55                  60

ggc tct gga gtc ccc agc cgc ttc tct gga tcc aaa gat gct tcg gcc aat gca ggg att      240
Gly Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile
                65                  70                  75                  80

                                                                CDR3
                                                    ------------------
tta ctc atc tct ggg ctc cag tct gag gat gag gct gac tat tac tgt atg att tgg cac      300
Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His
                85                  90                  95                  100

---------
agc agc gct tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt                      348
Ser Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
                105                 110                 115
```

FIG. 14

PM-2 Heavy chain variable region sequence

CDR1

```
ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agc tat gcc atg agc      60
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
 1               5                  10                  15                  20

                                                                  CDR2
tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca gct att agt ggt agt ggt     120
Trp val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp val Ser Ala Ile Aer Gly Ser Gly
                25                  30                  35                  40

ggt agt aca tac tac gca gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc     180
Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
                45                  50                  55                  60

aag aac acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac     240
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
                65                  70                  75                  80

                                CDR3
tgt gcg aaa ggt ggg gcc gaa ggc tgg tac gag tac tac tac tac tac ggt atg gac gtc     300
Cys Ala Lys Gly Gly Ala Glu Gly Trp Tyr Glu Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val
                85                  90                  95                  100

tgg ggc caa ggg acc ctg gtc                                                       321
Trp Gly Gln Gly Thr Leu Val
                105
```

FIG. 15

CM-2 Light chain variable region sequence

```
cag tct gcc ctg act cag cct gcc tcc gtg tct ggg tct cct gga cag tcg atc acc atc      60
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile
 1               5                  10                  15                  20
                                  CDR1
tcc tgc act gga acc agc agt gac gtt ggt ggt tat aac tat gtc tcc tgg tac caa cag     120
Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln
                25                  30                  35                  40
                                                CDR2
cac cca ggc aaa gcc ccc aaa ctc atg att tat gat gtc agt aat cgg ccc tca ggg gtt     180
His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val
                45                  50                  55                  60

tct aat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc tct gga ctc     240
Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
                65                  70                  75                  80
                                                CDR3
cag gct gag gac gag gct gat tac tac tgc agc tca aaa aga agc agc aac act cta gta     300
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Lys Arg Ser Ser Asn Thr Leu Val
                85                  90                  95                  100

ttc ggc gga ggg acc aag ctg acc gtc cta                                          330
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
                105                 110
```

FIG. 16

CM-2 Heavy chain variable region sequence

CDR1

```
aaa aag ccc ggg gag tct ctg agg atc tcc tgt aag ggc tct gga tac agt ttt acc acc      60
Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Thr
 1               5                  10                  15                  20

tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag tgg atg ggg atc atc     120
Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile
            25                  30                  35                  40
```

CDR2

```
tat cct ggt gac tct gat acc aga tac agc ccg tcc ttc caa ggc cag gtc acc atc tca     180
Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser
            45                  50                  55                  60

gcc gac acg tcc atc agt acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc     240
Ala Asp Thr Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr
            65                  70                  75                  80
```

CDR3

```
gcc ata tat tac tgt gcg agg gag gtc tat act ggc cga aac tac tac tac tac ggt ctg     300
Ala Ile Tyr Tyr Cys Ala Arg Glu Val Tyr Thr Gly Arg Asn Tyr Tyr Tyr Tyr Gly Leu
            85                  90                  95                  100

gac gtc tgg ggc caa gga acc ctg gtc                                                 327
Asp Val Trp Gly Gln Gly Thr Leu Val
            105
```

FIG. 17